

METHODS OF ENRICHING FOR AND IDENTIFYING POLYMORPHISMS

ABSTRACT OF THE DISCLOSURE

The invention encompasses methods for enriching for and identifying a polymorphism within a nucleic acid sample either by separating a subset of a nucleic acid sample or by selectively replicating a subset of a nucleic acid sample such that the polymorphism is contained within a nucleic acid population with reduced complexity, and then identifying the polymorphism within the enriched nucleic acid sample. Methods also are disclosed for enriching for and identifying a polymorphism by contacting a nucleic acid sample that includes a subset of nucleic acid molecules having a sequence that binds to a sequence-specific binding activity with a molecule having a sequence-specific binding activity under conditions which permit specific binding, such that the subset of nucleic acid molecules bound to the activity is enriched for nucleic acid molecules having the sequence recognized by the sequence-specific binding activity, and detecting a polymorphism with respect to a reference sequence in the subset of nucleic acid molecules.